



PCT10

RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/10/089,019

TIME: 16:07:33

Input Set : A:\USSEQLIST.TXT

Output Set: N:\CRF3\04112002\J089019.raw

ENTERED

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4 <110> APPLICANT: DEWOLF, WALTER E. JR
5   KALLENDER, HOWARD
6   LONSDALE, JOHN T.
8 <120> TITLE OF INVENTION: METHODS FOR MAKING AND USING FATTY ACID
9   SYNTHESIS PATHWAY REAGENTS
12 <130> FILE REFERENCE: GM50068
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/089,019
15 <141> CURRENT FILING DATE: 2002-03-25
17 <150> PRIOR APPLICATION NUMBER: PCT/US00/29451
18 <151> PRIOR FILING DATE: 2000-10-26
20 <150> PRIOR APPLICATION NUMBER: 60/161,775
21 <151> PRIOR FILING DATE: 1999-10-27
23 <160> NUMBER OF SEQ ID NOS: 37
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 999
29 <212> TYPE: DNA
30 <213> ORGANISM: Staphylococcus aureus
32 <400> SEQUENCE: 1
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34 catatgctcg agatgagtaa aacagcaatt atttttcccg gacaagggtgc ccaaaaagtt 120
35 ggtatggcac aagatttgtt taataacaat gatcaagcaa ctgaaatttt aacttcagca 180
36 gcaaagacgt tagactttga tatttttagag acaatgttta ctgatgaaga aggtaaattg 240
37 ggtgaaactg aaaacacgca accagcttta ttgacgcata gttcggcatt attagcagcg 300
38 ctaaaaaattt tgaatcctga ttttactatg gggcatagtt taggtgaata ttcaagttta 360
39 gttgcagctg acgtattatc atttgaagat gcagttaaaa ttgttagaaa acgtgggtcaa 420
40 ttaatggcgc aagcatttcc tactgggtga ggaagcatgg ctgcagtatt gggattagat 480
41 tttgataaag tcgatgaaat ttgtaagtca ttatcatctg atgacaaaaat aattgaacca 540
42 gcaaacatta attgcccagg tcaaattggt gtttcagggtc acaaagcttt aattgatgag 600
43 ctagtagaaa aaggtaaatc attaggtgca aaacgtgtca tgccttttagc agtatctgga 660
44 ccattccatt catcgcta at gaaagtgatt gaagaagatt tttcaagtta cattaatcaa 720
45 tttgaatggc gtgatgctaa gtttcctgta gttcaaaatg taaatgcgca aggtgaaact 780
46 gacaaagaag taattaaatc taatatgggtc aagcaattat attcaccagt acaattcatt 840
47 aactcaacag aatggcta at agaccaaggt gttgatcatt ttattgaaat tggtcctgga 900
48 aaagttttat ctggctta at taaaaaata aatagagatg ttaagttaac atcaattcaa 960
49 actttagaag atgtgaaagg atggaatgaa aatgactaa 999
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 332
53 <212> TYPE: PRT
54 <213> ORGANISM: Staphylococcus aureus
56 <400> SEQUENCE: 2
57 Met Gly His His His His His His His His His Ser Ser Gly His
58 1 5 10 15

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59 Ile Glu Gly Arg His Met Leu Glu Met Ser Lys Thr Ala Ile Ile Phe
60      20      25      30
61 Pro Gly Gln Gly Ala Gln Lys Val Gly Met Ala Gln Asp Leu Phe Asn
62      35      40      45
63 Asn Asn Asp Gln Ala Thr Glu Ile Leu Thr Ser Ala Ala Lys Thr Leu
64      50      55      60
65 Asp Phe Asp Ile Leu Glu Thr Met Phe Thr Asp Glu Glu Gly Lys Leu
66 65      70      75      80
67 Gly Glu Thr Glu Asn Thr Gln Pro Ala Leu Leu Thr His Ser Ser Ala
68      85      90      95
69 Leu Leu Ala Ala Leu Lys Ile Leu Asn Pro Asp Phe Thr Met Gly His
70      100     105     110
71 Ser Leu Gly Glu Tyr Ser Ser Leu Val Ala Ala Asp Val Leu Ser Phe
72      115     120     125
73 Glu Asp Ala Val Lys Ile Val Arg Lys Arg Gly Gln Leu Met Ala Gln
74      130     135     140
75 Ala Phe Pro Thr Gly Val Gly Ser Met Ala Ala Val Leu Gly Leu Asp
76 145     150     155     160
77 Phe Asp Lys Val Asp Glu Ile Cys Lys Ser Leu Ser Ser Asp Asp Lys
78      165     170     175
79 Ile Ile Glu Pro Ala Asn Ile Asn Cys Pro Gly Gln Ile Val Val Ser
80      180     185     190
81 Gly His Lys Ala Leu Ile Asp Glu Leu Val Glu Lys Gly Lys Ser Leu
82      195     200     205
83 Gly Ala Lys Arg Val Met Pro Leu Ala Val Ser Gly Pro Phe His Ser
84      210     215     220
85 Ser Leu Met Lys Val Ile Glu Glu Asp Phe Ser Ser Tyr Ile Asn Gln
86 225     230     235     240
87 Phe Glu Trp Arg Asp Ala Lys Phe Pro Val Val Gln Asn Val Asn Ala
88      245     250     255
89 Gln Gly Glu Thr Asp Lys Glu Val Ile Lys Ser Asn Met Val Lys Gln
90      260     265     270
91 Leu Tyr Ser Pro Val Gln Phe Ile Asn Ser Thr Glu Trp Leu Ile Asp
92      275     280     285
93 Gln Gly Val Asp His Phe Ile Glu Ile Gly Pro Gly Lys Val Leu Ser
94      290     295     300
95 Gly Leu Ile Lys Lys Ile Asn Arg Asp Val Lys Leu Thr Ser Ile Gln
96 305     310     315     320
97 Thr Leu Glu Asp Val Lys Gly Trp Asn Glu Asn Asp
98      325     330
101 <210> SEQ ID NO: 3
102 <211> LENGTH: 312
103 <212> TYPE: PRT
104 <213> ORGANISM: Staphylococcus aureus
106 <400> SEQUENCE: 3
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108 1      5      10      15
109 Ala Gln Lys Val Gly Met Ala Gln Asp Leu Phe Asn Asn Asn Asp Gln
110      20      25      30

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111 Ala Thr Glu Ile Leu Thr Ser Ala Ala Lys Thr Leu Asp Phe Asp Ile
112          35          40          45
113 Leu Glu Thr Met Phe Thr Asp Glu Glu Gly Lys Leu Gly Glu Thr Glu
114          50          55          60
115 Asn Thr Gln Pro Ala Leu Thr His Ser Ser Ala Leu Leu Ala Ala
116 65          70          75          80
117 Leu Lys Ile Leu Asn Pro Asp Phe Thr Met Gly His Ser Leu Gly Glu
118          85          90          95
119 Tyr Ser Ser Leu Val Ala Ala Asp Val Leu Ser Phe Glu Asp Ala Val
120          100          105          110
121 Lys Ile Val Arg Lys Arg Gly Gln Leu Met Ala Gln Ala Phe Pro Thr
122          115          120          125
123 Gly Val Gly Ser Met Ala Ala Val Leu Gly Leu Asp Phe Asp Lys Val
124          130          135          140
125 Asp Glu Ile Cys Lys Ser Leu Ser Ser Asp Asp Lys Ile Ile Glu Pro
126 145          150          155          160
127 Ala Asn Ile Asn Cys Pro Gly Gln Ile Val Val Ser Gly His Lys Ala
128          165          170          175
129 Leu Ile Asp Glu Leu Val Glu Lys Gly Lys Ser Leu Gly Ala Lys Arg
130          180          185          190
131 Val Met Pro Leu Ala Val Ser Gly Pro Phe His Ser Ser Leu Met Lys
132          195          200          205
133 Val Ile Glu Glu Asp Phe Ser Ser Tyr Ile Asn Gln Phe Glu Trp Arg
134          210          215          220
135 Asp Ala Lys Phe Pro Val Val Gln Asn Val Asn Ala Gln Gly Glu Thr
136 225          230          235          240
137 Asp Lys Glu Val Ile Lys Ser Asn Met Val Lys Gln Leu Tyr Ser Pro
138          245          250          255
139 Val Gln Phe Ile Asn Ser Thr Glu Trp Leu Ile Asp Gln Gly Val Asp
140          260          265          270
141 His Phe Ile Glu Ile Gly Pro Gly Lys Val Leu Ser Gly Leu Ile Lys
142          275          280          285
143 Lys Ile Asn Arg Asp Val Lys Leu Thr Ser Ile Gln Thr Leu Glu Asp
144          290          295          300
145 Val Lys Gly Trp Asn Glu Asn Asp
146 305          310
149 <210> SEQ ID NO: 4
150 <211> LENGTH: 1001
151 <212> TYPE: DNA
152 <213> ORGANISM: Staphylococcus aureus
154 <400> SEQUENCE: 4
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156 atgaacgtgg gtattaaagg ttttgggtgca tatgcaccag aaaagattat tgacaatgcc 120
157 tatttttgagc aatttttaga tacatctgat gaatggattt ctaagatgac tggaattaaa 180
158 gaaagacatt gggcagatga cgatcaagat acttcagatt tagcatatga agcaagtgtg 240
159 aaagcaatcg ctgacgctgg tattcagcct gaagatatag atatgataat tgttgccaca 300
160 gcaactggag atatgccatt tccaactgtc gcaaatatgt tgcaagaacg tttagggacg 360
161 ggcaaagttg cctctatgga tcaacttgca gcatgttctg gatttatgta ttcaatgatt 420
162 acagctaaac aatatgttca atctggagat tatcataata ttttagttgt cgggtgcagat 480

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163 aaattatcta aaataacaga ttttaactgac cgtttctactg cagtttctatt tggagatggg 540
164 gcagggtgcgg ttatcatcgg tgaagtttca gaaggcagag gtattataag ttatgaaatg 600
165 ggtttctgatg gcaactgggtg taaacattta tatttagata aagatactgg taaactgaaa 660
166 atgaatggtc gagaagtatt taaatttgct gttagaatta tgggtgatgc atcaacacgt 720
167 gtagttgaaa aagcgaattt aacatcagat gatatagatt tatttattcc tcatcaagct 780
168 aatattagaa ttatggaatc agctagagaa cgcttaggta tttcaaaaga caaatgagt 840
169 gttttctgtaa ataaatatgg aaatacttca gctgcgtcaa tacctttaag tatcgatcaa 900
170 gaattaaaaa atggtaaact caaagatgat gatacaattg ttcttgctcg attcgggtggc 960
171 ggcctaactt ggggcgcaat gacaataaaa tggggaaaat a 1001
173 <210> SEQ ID NO: 5
174 <211> LENGTH: 333
175 <212> TYPE: PRT
176 <213> ORGANISM: Staphylococcus aureus
178 <400> SEQUENCE: 5
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180 1 5 10 15
181 Arg Gly Ser His Met Asn Val Gly Ile Lys Gly Phe Gly Ala Tyr Ala
182 20 25 30
183 Pro Glu Lys Ile Ile Asp Asn Ala Tyr Phe Glu Gln Phe Leu Asp Thr
184 35 40 45
185 Ser Asp Glu Trp Ile Ser Lys Met Thr Gly Ile Lys Glu Arg His Trp
186 50 55 60
187 Ala Asp Asp Asp Gln Asp Thr Ser Asp Leu Ala Tyr Glu Ala Ser Val
188 65 70 75 80
189 Lys Ala Ile Ala Asp Ala Gly Ile Gln Pro Glu Asp Ile Asp Met Ile
190 85 90 95
191 Ile Val Ala Thr Ala Thr Gly Asp Met Pro Phe Pro Thr Val Ala Asn
192 100 105 110
193 Met Leu Gln Glu Arg Leu Gly Thr Gly Lys Val Ala Ser Met Asp Gln
194 115 120 125
195 Leu Ala Ala Cys Ser Gly Phe Met Tyr Ser Met Ile Thr Ala Lys Gln
196 130 135 140
197 Tyr Val Gln Ser Gly Asp Tyr His Asn Ile Leu Val Val Gly Ala Asp
198 145 150 155 160
199 Lys Leu Ser Lys Ile Thr Asp Leu Thr Asp Arg Ser Thr Ala Val Leu
200 165 170 175
201 Phe Gly Asp Gly Ala Gly Ala Val Ile Ile Gly Glu Val Ser Glu Gly
202 180 185 190
203 Arg Gly Ile Ile Ser Tyr Glu Met Gly Ser Asp Gly Thr Gly Gly Lys
204 195 200 205
205 His Leu Tyr Leu Asp Lys Asp Thr Gly Lys Leu Lys Met Asn Gly Arg
206 210 215 220
207 Glu Val Phe Lys Phe Ala Val Arg Ile Met Gly Asp Ala Ser Thr Arg
208 225 230 235 240
209 Val Val Glu Lys Ala Asn Leu Thr Ser Asp Asp Ile Asp Leu Phe Ile
210 245 250 255
211 Pro His Gln Ala Asn Ile Arg Ile Met Glu Ser Ala Arg Glu Arg Leu
212 260 265 270
213 Gly Ile Ser Lys Asp Lys Met Ser Val Ser Val Asn Lys Tyr Gly Asn

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214          275          280          285
215 Thr Ser Ala Ala Ser Ile Pro Leu Ser Ile Asp Gln Glu Leu Lys Asn
216          290          295          300
217 Gly Lys Leu Lys Asp Asp Thr Ile Val Leu Val Gly Phe Gly Gly
218 305          310          315          320
219 Gly Leu Thr Trp Gly Ala Met Thr Ile Lys Trp Gly Lys
220          325          330
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 315
225 <212> TYPE: PRT
226 <213> ORGANISM: Staphylococcus aureus
228 <400> SEQUENCE: 6
229 Gly Ser His Met Asn Val Gly Ile Lys Gly Phe Gly Ala Tyr Ala Pro
230 1          5          10          15
231 Glu Lys Ile Ile Asp Asn Ala Tyr Phe Glu Gln Phe Leu Asp Thr Ser
232          20          25          30
233 Asp Glu Trp Ile Ser Lys Met Thr Gly Ile Lys Glu Arg His Trp Ala
234          35          40          45
235 Asp Asp Asp Gln Asp Thr Ser Asp Leu Ala Glu Ala Ser Val Lys Ala
236          50          55          60
237 Ile Ala Asp Ala Gly Ile Gln Pro Glu Asp Ile Asp Met Ile Ile Val
238 65          70          75          80
239 Ala Thr Ala Thr Gly Asp Met Pro Phe Pro Thr Val Ala Asn Met Leu
240          85          90          95
241 Gln Glu Arg Leu Gly Thr Gly Lys Val Ala Ser Met Asp Gln Leu Ala
242          100          105          110
243 Ala Cys Ser Gly Phe Met Tyr Ser Met Ile Thr Ala Lys Gln Tyr Val
244          115          120          125
245 Gln Ser Gly Asp Tyr His Asn Ile Leu Val Val Gly Ala Asp Lys Leu
246          130          135          140
247 Ser Lys Ile Thr Asp Leu Thr Asp Arg Ser Thr Ala Val Leu Phe Gly
248 145          150          155          160
249 Asp Gly Ala Gly Ala Val Ile Ile Gly Glu Val Ser Glu Gly Arg Gly
250          165          170          175
251 Ile Ile Ser Tyr Glu Met Gly Ser Asp Gly Thr Gly Gly Lys His Leu
252          180          185          190
253 Tyr Leu Asp Lys Asp Thr Gly Lys Leu Lys Met Asn Gly Arg Glu Val
254          195          200          205
255 Phe Lys Phe Ala Val Arg Ile Met Gly Asp Ala Ser Thr Arg Val Val
256          210          215          220
257 Glu Lys Ala Asn Leu Thr Ser Asp Asp Ile Asp Leu Phe Ile Pro His
258 225          230          235          240
259 Gln Ala Asn Ile Arg Ile Met Glu Ser Ala Arg Glu Arg Leu Gly Ile
260          245          250          255
261 Ser Lys Asp Lys Met Ser Val Ser Val Asn Lys Tyr Gly Asn Thr Ser
262          260          265          270
263 Ala Ala Ser Ile Pro Leu Ser Ile Asp Gln Glu Leu Lys Asn Gly Lys
264          275          280          285
265 Leu Lys Asp Asp Asp Thr Ile Val Leu Val Gly Phe Gly Gly Gly Leu

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VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number